

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1447.31 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-102
Perfect score: 1410
Sequence: 1 atgaagaacaacatctggt.....cttactacctgtgtaataa 1410

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_estba:*
3: em_estba:*
4: em_estba:*
5: em_estba:*
6: em_estba:*
7: em_estba:*
8: em_estba:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rpd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	57.2	4.1	502	14 BQ134889	BQ134889 INIT1_1_D
C 2	57.2	4.1	590	14 BQ135179	BQ135179 INIT1_4_C
C 3	57.2	4.1	602	14 BQ135164	BQ135164 INIT1_4_B
C 4	57.2	4.1	607	14 BQ134912	BQ134912 INIT1_1_F
C 5	56.8	4.0	658	14 BQ135057	BQ135057 INIT1_2_G
C 6	54	3.8	445	14 BQ134871	BQ134871 INIT1_1_B

C 7	52.4	3.7	419	14 BQ135036	BQ135036 INIT1_2_D
C 8	40	2.8	210	14 BQ134900	BQ134900 INIT1_1_E
C 9	40	2.8	538	14 BQ134810	BQ134810 INIT1_4_C
C 10	40	2.8	592	14 BQ134985	BQ134985 INIT1_2_G
C 11	40	2.8	599	14 BQ134821	BQ134821 INIT1_4_D
C 12	40	2.8	661	14 BQ135189	BQ135189 INIT1_4_D
C 13	40	2.8	675	14 BQ135196	BQ135196 INIT1_4_E
C 14	40	2.8	856	9 AL529709	AL529709 AL529709
C 15	39.8	2.8	565	12 BF191747	BF191747 239419 MA
C 16	39.4	2.8	946	17 CNS06063	AL10257 T7 end of
C 17	38.6	2.7	938	13 BI950738	BI950738 HVSME1002
C 18	37.8	2.7	390	13 BI316601	BI316601 saf0509.
C 19	37.8	2.7	997	17 CNS06066	AL11124 T7 end of
C 20	37.8	2.7	1089	17 CNS06P2J	AL10021 T3 end of
C 21	37.6	2.7	479	12 BF776376	BF776376 287167 MA
C 22	37.4	2.7	413	12 BG156079	BI156079 saa80a12.
C 23	37.4	2.7	977	17 CNS02AMA	AL188731 Tetraodon
C 24	37.2	2.6	941	17 CNS056AV	AL323104 Tetraodon
C 25	37	2.6	1177	13 BG915930	BG915930 602815385
C 26	36.8	2.6	877	17 CNS04NMK	AL299261 Tetraodon
C 27	36.6	2.6	328	10 BB497602	BB497602 BB497602
C 28	36.4	2.6	576	9 AL818926	AL818926 AL818926
C 29	36.2	2.6	389	10 AW325085	AW325085 TENUA4390
C 30	36.2	2.6	448	12 BF255972	BF255972 HVSMEF000
C 31	36.2	2.6	473	13 BM098087	BM098087 EBP103 SQ
C 32	36.2	2.6	576	12 BG301223	BG301223 HVSMEB001
C 33	36.2	2.6	688	9 AJ612588	AJ612588 TENG0393
C 34	36.2	2.6	791	9 AJ443260	AJ443260 AJ443260
C 35	36.2	2.6	894	12 BG367203	BG367203 HVSME1001
C 36	35.8	2.5	256	12 BG301587	BG301587 kt02h09.Y
C 37	35.8	2.5	273	13 BM339376	BM339376 MEST240-F
C 38	35.8	2.5	424	9 A1438101	A1438101 sa35h11.Y
C 39	35.8	2.5	447	12 BF707190	BF707190 282711.MA
C 40	35.8	2.5	513	10 BE355071	BE355071 BG1113-G
C 41	35.8	2.5	654	13 BI874624	BI874624 963116H11
C 42	35.8	2.5	669	9 AU169066	AU169066 AU169066
C 43	35.8	2.5	713	17 AZ346186	AZ346186 1M0081G06
C 44	35.8	2.5	862	12 BG769770	BG769770 602744673
C 45	35.8	2.5	920	12 BG420157	BG420157 602452258

ALIGNMENTS

RESULT 1
BQ134889/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ134889 502 bp mRNA linear EST 22-APR-2002
INIT1_1_D07.bl_A006.G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
BQ134889
BQ134889.1 GI:20260988
EST.
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 502)
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 474

Seq primer: T7
High quality sequence start: 43
High quality sequence stop: 590
POLYA=No.

FEATURES
source Location/Qualifiers
1..590
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="c5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 207 a 103 c 94 g 186 t
ORIGIN
Query Match 4.1%; Score 57.2; DB 14; Length 590;
Best Local Similarity 52.0%; Pred. No. 0.00013;
Matches 159; Conservative 0; Mismatches 138; Indels 9; Gaps 1;
QY 1114 GCTACCTGATCGTCAGTGTCTGAGTGTCTGGAACCGTCTGACCGACGGA 1173
Db 379 GCTACTTCAGCCACATAATGTTAAACGATTGCCCTGCTGGTACAGTGGTTGATGATGGT 320
QY 1174 ACCACCTCTACCTACACGAGCGTCTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
Db 313 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGCTAAATGTTAGGCTAACTTTTAT 254
QY 1234 ACCACCAAGCAGACCGAGTGGTGGTGGATCGACACCTGTACCTCTGTAAACAAGAG 1293
Db 253 GCATCAAAAACATCTGGTTTTCAGCAGGACTGATGATGATGATGATGATGATGATGATG 194
QY 1294 CTGACCTCGGAGTGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
Db 193 TTAACCTTCGTGCTACAGCTAAAGTATATGCTGAAGTACTTAAAGACATAATGCGCC 134
QY 1354 -----TTGCGTAACTTCCTGCTCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
Db 133 AGTTCCACTTTTCGAAAAATTTTATCAATGCTCTTAATATTTTCTTTCTTTCTTTG 74
QY 1405 TAATAA 1410
Db 73 TGATGA 68

RESULT 3
BQ135164/c
LOCUS
DEFINITION
BQ135164 602 bp mRNA linear EST 22-APR-2002
INIT1_4_B05.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
BQ135164
ACCESSION
BQ135164.1 GI:20261263
VERSION
BQ135164.1
KEYWORDS
EST.
SOURCE
Ichthyophthirius multifiliis.
ORGANISM
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 602)
AUTHORS
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Contact: Cordonnier-Pratt MM
Unpublished (2002)
TITLE
Laboratory for Genomics and Bioinformatics
JOURNAL
The University of Georgia, Department of Plant Biology
COMMENT
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

POLYA=Yes.

FEATURES
source Location/Qualifiers
1..502
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 185 a 80 c 70 g 167 t
ORIGIN
Query Match 4.1%; Score 57.2; DB 14; Length 502;
Best Local Similarity 52.0%; Pred. No. 0.00012;
Matches 159; Conservative 0; Mismatches 138; Indels 9; Gaps 1;
QY 1114 GCTACCTGATCGTCAGTGTCTGAGTGTCTGGAACCGTCTGACCGACGGA 1173
Db 379 GCTACTTCAGCCACATAATGTTAAACGATTGCCCTGCTGGTACAGTGGTTGATGATGGT 320
QY 1174 ACCACCTCTACCTACACGAGCGTCTCTGAGTGTGTGAAGTGTGCTTAACCTTCTAC 1233
Db 313 ACATCAACTAATTTTGTAGCTTTAGCAAGTGAATGCTAAATGTTAGGCTAACTTTTAT 260
QY 1234 ACCACCAAGCAGACCGAGTGGTGGTGGATCGACACCTGTACCTCTGTAAACAAGAG 1293
Db 253 GCATCAAAAACATCTGGTTTTCAGCAGGACTGATGATGATGATGATGATGATGATGATG 200
QY 1294 CTGACCTCGGAGTGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1353
Db 193 TTAACCTTCGTGCTACAGCTAAAGTATATGCTGAAGTACTTAAAGACATAATGCGCC 140
QY 1354 -----TTGCGTAACTTCCTGCTCTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1404
Db 139 AGTTCCACTTTTCGAAAAATTTTATCAATGCTCTTAATATTTTCTTTCTTTCTTTG 80
QY 1405 TAATAA 1410
Db 79 TGATGA 74

RESULT 2
BQ135179/c
LOCUS
DEFINITION
BQ135179 590 bp mRNA linear EST 22-APR-2002
INIT1_4_C08.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
BQ135179
ACCESSION
BQ135179.1 GI:20261278
VERSION
BQ135179.1
KEYWORDS
EST.
SOURCE
Ichthyophthirius multifiliis.
ORGANISM
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE
1 (bases 1 to 590)
AUTHORS
Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Contact: Cordonnier-Pratt MM
Unpublished (2002)
TITLE
Laboratory for Genomics and Bioinformatics
JOURNAL
The University of Georgia, Department of Plant Biology
COMMENT
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.

The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: T7
High quality sequence start: 67
High quality sequence stop: 658
POLYA=No.

FEATURES

source

Location/Qualifiers

1..658 /organism="Ichthyophthirius multifiliis"

/strain="G5"

/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 215 a 122 c 122 g 199 t

ORIGIN

Query Match 4.0%; Score 56.8; DB 14; Length 658;

Best Local Similarity 52.0%; Pred. No. 0.00018;

Matches 158; Conservative 0; Mismatches 137; Indels 9; Gaps 1;

QY 1114 GCTACCTGATGCTCAGTGTCTGGAGTGCCTGGAGACCTGCTGACCGACGGA 1173

DB 315 GCTATTCAGCCACATAATTTAAACGATTCGCCCTGCTGGTACAGTGGTGTGATGGT 256

QY 1174 ACCACCTCTACCTACAGCAGGCTGCTCTGAGTGTGTGAAGTGTGCTGCTACTTCTAC 1233

DB 255 ACATCACTAATTTTGTAGCTTTAGCAAGTGAATGACTAAATGTTAGGCTACTTTTAT 196

QY 1234 ACCACCAAGCAGCAGCTGGTGGTGGTGAATCGACACCTGTACCTCTTGTACACAGAAG 1293

DB 195 GCATCAAAAACATCTGTTTTCAGCAGGACTGATCATATGTAATGTTCTTAAAAA 136

QY 1294 CTGACCTCTGAGCTGAGGCTAACCTCCCTGAGTCTGCTGAAGAACAACATCCAGTGTGAC 1353

DB 135 TTAACCTCTGTGTACAGCTAAAGTATATGCTGAAGTACTTAAAGACATAATGCGCC 76

QY 1354 -----TTCGCTAACTTCCTGTCTATCTCTGCTGTCTGCTGTCTTACTACCTGCTG 1404

DB 75 AGTTCCACTTCGCAAAATTTTATCAATGCTCTTAATATTTATTTCTTCTATTGTTG 16

QY 1405 TAAT 1408

DB 15 TGAT 12

RESULT 6

B0134871/c

LOCUS INIT1_LB05.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius

multifiliis cDNA, mRNA sequence.

ACCESSION B0134871

VERSION B0134871.1

KEYWORDS EST.

SOURCE B0134871.1 GI:20260970

ORGANISM Ichthyophthirius multifiliis.

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 445)

REFERENCE Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,

Dickerson,H., Lin,T.-L. and Pratt,L.H.

TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)

JOURNAL COMMENT

Unpublished (2002)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV

High quality sequence start: 37

High quality sequence stop: 443

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..445 /organism="Ichthyophthirius multifiliis"

/strain="G5"

/db_xref="taxon:5932"

/clone_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 155 a 79 c 71 g 140 t

ORIGIN

Query Match 3.8%; Score 54; DB 14; Length 445;

Best Local Similarity 51.3%; Pred. No. 0.00084;

Matches 157; Conservative 0; Mismatches 140; Indels 9; Gaps 1;

QY 1114 GCTACCTGTACCTACAGCAGGCTGCTCTGAGTGTGTGAAGTGTGCTGCTTAACCTTCTAC 1173

DB 323 GCTACTTCAGCCACATAATGTTAAACGATTCGCCCTGCTGGTACAGTGGTGTGATGGT 264

QY 1174 ACCACCTCTACCTACAGCAGGCTGCTCTGAGTGTGTGAAGTGTGCTGCTTAACCTTCTAC 1233

DB 263 TCATCACTAATTTTGTAGCTTTAGCAAGTGAATGCTCTAAATGTTAGGCTAACTTTAT 204

QY 1234 ACCACCAAGCAGCAGCTGGTGGTGGTGAATCGACACCTGTACCTCTGCTTAACCAAGAAG 1293

DB 203 GCATCAAAAACATCTGTTTTCAGCAGGACTGATGATGATGCTGAATGTTCTTAAAAA 144

QY 1294 CTGACCTCTGGAGCTGAGGCTAACCTGCTGAGTCTGCTGAAGAACAACATCCAGTGTGAC 1353

DB 143 TTAACCTTTGGTGTACAGCTAAAGTATATGCTGAAGTACTTAAAAAGCATAATGCGCC 84

QY 1354 -----TTCGCTAACTTCCTGTCTATCTCTGCTGTCTGCTGTCTTACTACCTGCTG 1404

DB 83 AGTTCCACTTCGCAAAATTTTATCAATGCTCTTAATATTTTCTTCTATTGCGG 24

QY 1405 TAATAA 1410

DB 23 TGATGA 18

RESULT 7

B0135036/c

LOCUS INIT1_L2D10.gL_A006 G5 trophont cDNA (INIT1) Ichthyophthirius

multifiliis cDNA, mRNA sequence.

ACCESSION B0135036

VERSION B0135036.1

KEYWORDS EST.

SOURCE B0135036.1 GI:20261135

ORGANISM Ichthyophthirius multifiliis.

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Ophryoglenina; Ichthyophthirius.

1 (bases 1 to 419)

REFERENCE


```

source
1. .565
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2Pig"
/tissue_type="pooled"
/lab_host="DH10B"
/notes=vector; pcwv sport6; site_1: NotI; Site_2: SalI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
115 a 147 c 161 g 141 t 1 others

```

[illegible]

D0	375	ATGTCCTGCTGGAACCGTGCTGACCGACGGAACACCTTACCTTCAAGCAGGCTGCTT	1201
Qy	1142	AGTGTCTGCTGGAACCGTGCTGACCGACGGAACACCTTACCTTCAAGCAGGCTGCTT	
Db	433	TTTGTCTGTTGTTCAGGCGTTTGCCAGGCAGATACCCCTTCTGTACCCGGAGT	492
Qy	1202	CTGAGTGTGTGAAAGT	1217
Db	493	TTCCGTGGACGAGCTG	508

[illegible]

RESULT 15				
BF191747	BF191747	565 bp	mRNA	linear
LOCUS	239419			
DEFINITION	MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.			
				EST 02-NOV-2000

DERIVATION	BF191747	GI:11075116
ACCESSION	BF191747.1	
VERSION	EST.	
KEYWORDS	EST.	
SOURCE	pic	

ORGANISM	F-3
Sus scrofa	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
REFERENCE	1 (bases 1 to 565)

AUTHORS	TITLE
Fahrenkrug, S.C., Fekking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.	Design and use of two pooled tissue normalized cDNA libraries for

EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, APIS, IIS Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred v0.980904 e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

FORWARD: AGGAACACGCTATGACCAT
 BACKWARD: GTTTTCCCACTCAGCAGC
 Plate: 67 row: 0 column: 16
 Seq primer: ATTTAGGTGACACTATAG.

FEATURES	Location/Qualifiers
• • • • •	